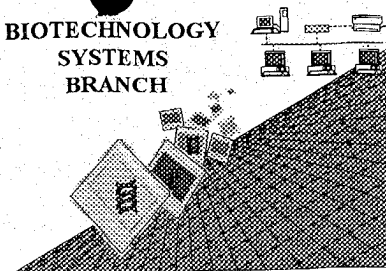


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0590  
10/9

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/761,142  
Source: O/PE  
Date Processed by STIC: 1/30/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001

TIME: 11:19:35

Input Set : A:\31133A.ST25.txt

Output Set: N:\CRF3\01302001\I761142.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:1221 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
 L:1221 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
 L:1221 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
 L:1221 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
 L:1221 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26  
 L:1285 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
 L:1285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
 L:1285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
 L:1285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
 M:340 Repeated in SeqNo=26  
 L:1286 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
 L:1286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
 L:1286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
 L:1286 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
 L:1287 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
 L:1287 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
 L:1287 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
 L:1287 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
 L:1839 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32  
 L:1839 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32  
 L:1839 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32  
 L:1839 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32  
 L:1839 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32  
 L:11047 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:153  
 L:11047 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:153  
 L:11047 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:153  
 L:11047 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:153  
 L:11047 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:153  
 L:19618 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:258  
 L:19618 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:258  
 L:19618 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:258  
 L:19618 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:258  
 L:19618 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:258  
 L:28080 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:356  
 L:28080 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:356  
 L:28080 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:356  
 L:28080 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:356  
 L:28080 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:356

<210> 26  
 <211> 6413  
 <212> DNA  
 <213> Drosophila melanogaster

<400> 26

```

gaattccttc acaggcgggt tcttggccgc attatcggtta atattgttgt tggacatgta 60
cagctcgcat tgctgcacta ttttatccaa ttttcgaatt tcgctcagtt ccacgcaaga 120
tttgtgggac atttttaagt ctgcaaagta tagaaacgaa aaagtgttgc aaattataat 180
caaacattcg caaagctcag aatatccgga ttcgtaagca aattcaaata aatcttcgct 240
taaaaaacaac ttaataataa atccaaaatt tccacttact ccagattgaa attggcgaaa 300
actgcgattt cttacctaata gcacttttctt atttactttgc aaatcaaaac agaacaggta 360
tgacatgcac gcggagaaat caggagtggg aaatcatttt caatcaatta aaaacacttc 420
aattcgatct tgttcgttac acatactcta ctttttaaat atcatagata aaataaaaaa 480
atgaatagat gtatgtaaat acatggcatt ttcatttcga agtcaactgc tttataagac 540
caactttttt ttcccggtgt aatcaggcctt tgcttttctg aaattttcag acatgcgtac 600
tgctttcggg tttcaaagat tcgaaaccac cgtgattttc gaaccattgt tattttcctt 660
ctcgcattcg gtcacactat tttcaaacgt aaacaattga tttttcctgc taaacaaaag 720
tggttgaaaa tgctcggaat cgctgccaaa aagattgccg aagcggagga cctgggtgaag 780
caggccgaga agaggtatcc ccaacaaaaa tatccttata aaggggtttc caaataacac 840
ccatctttat ttgcagcttg aagttgtcca tgctgaaatg gggttcctgat tacgatagt 900
ctgcggatga gtattccaaa gctggtgagt ttcacaaagt aggagtgact aatatcacc 960
agagtatcta tctataaaaa cattgtgaca tcaatgagat atgtaaatac tatgaattac 1020
agctaacgat tatcccaaag tatccataac ttgcaagata cacacatatt ggtgtacaat 1080
tatgtatctt tcttttacat ttttaattgc agccactgca tatcgaatag ctaaaagtta 1140
tgataagagc aaggagtgtt ttctgaaggc aatcgacgcc tataaaaaa acaagtcttg 1200
gttccatgct gcaaaggcat acgaacaggt gagcttaaat tgaagttaat ataagtgaag 1260
ttaataggaa atttaaacc tctaaatgtg cacatcttct agatcatttt gctgtcaaag 1320
gatgccgata agctacacga agttgaggaa tacgccaaaca aatcggcgag tttgtatcaa 1380
cagcacgggt cccagaggc agccgcatcc gccttgata aagccgcaa gttaactgaa 1440
tccaagcatc ctgacatggc tttgcgcttc tatcagcatg ctctagaagt cataatggtt 1500
cgtcctattht gacactgctc tagtcaattc cattcttaaa ctattaattt tatacttacc 1560
cgacagatcg aggattccgt ccgtcaagca gccgagtatg atcaaaaagt tccaggatac 1620
tggtcaaact aaggaggtat gtacctatga ttgcaacgaa tcactttggg tatccttagc 1680
ttatatcatc caatcactcc aggtacgacg aagccacgaa tgcgctcaa aaggagatca 1740
gcttgaatca gcaaacggaa tcttacggac aaattggacg cctagtgtgt gccttggtga 1800
tggtccaact ggctcgcggt gattccgtgg aagccgaaaa gaccttcagg gagtggggaa 1860
actgctgcga gccagaggaa gtgtccacac tgcagaccct tctgcaagcc ttcgatgacg 1920
aggatcccg gttagctgct aggatgctgg catccctatt catacgacat atggatgttg 1980
agtacgctat tctatctaaa aacattccac tacctcaggg tatacagatg gagaagaagg 2040
ctggcgacac tgctgctgtg agtattttta ttctaaaaat ggaatttgca atttttgttt 2100

```

→ see  
 item 10 on  
 Error Summary  
 sheet

( Partial listing of Sequence 26 - due to  
 size of sequence, only first error shown -  
 similar errors exist in the rest of the  
 sequence)

FYI

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001  
 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set : N:\CRF3\01302001\I761142.raw

```

275 atttacoggg cgtaagacc caccgaatgc ggtaattta agtgataata taatatatta 420
276 aataagaata tgtaataacg tgtaccctgt gacaaatglt tacagtctct aactaatctg 480
277 tactttcgta ttttacaaga acgtaaacgt acgatatcag agtatctaaa agtaaaacca 540
278 cgaatcgttc atgtttacgg tttacggatt acgagtaaaa tggatatcaa tcttttgatc 600
279 aactacctat cgaccattac agactgacgg tttacattca acttttttac tgcgacatct 660
280 gcgattactt agcacgaaca taaataaata aaccgtgggg tegtgatgtg caggttaaat 720
281 aataaatttc acgaacagcg ccgtaatttt ataataatcc agtoatgttt tacatataaa 780
282 tctgaaactt cgaccgacta gttgctaaat tattcattga aagtggataa tttttattat 840
283 ttggggatttt gataatgcgg aatagccatc cacaatttat tattacgtaa ggtatatcga 900
284 tcaaggactt caagtatcgg tgttggaacc gttcattaaa taattcaata acccgggtgt 960
285 gaaaatcaaa atcaaaagatt gagacgctct tctacaagc aagttcttct ttatctaate 1020
286 ctteattaaa tcaggtatta aaaggaaatc tgattcctga attgattgat aaaacaaagg 1080
287 gaaagcaagt ctgcacgttg cacaagaaga agaggacacc gcactggtgg accccaagcc 1140
288 ggcagaggca gatgcgctcg ataccagacc gtgaaacgcc tctctgctca aagcctcagc 1200
289 ggaaggaccc gtacatgcac cggaaacttc acagcatgtt cataaggtat atgcactcat 1260
290 ttgacgcaag tgttgacgtt cagtgtctga ttggagaaac gtaagtcagt gattaaacgt 1320
291 caccggacca atatcgcgcg gaccggagga tggagaagtg gaagtgcgcg tacgcctcgc 1380
292 tgcactaccc gtccaagctc ctgcgctacg cgtcggaaga gctcgcttct tgggtgtcgc 1440
293 tgcgttctca cgtcggtcac gtgtcggaag agccgacgac gccgtaaact cctggcgctc 1500
294 tgatggaagt cctcctcgtg ccgcgggagc ggtcgtcgac gacgatgcgg aagctgacga 1560
295 ggttcggcgg cgtgcagatg ctctccctca cgaggtggtt ccgccatcga tgagactctt 1620
296 acgtccgctt cgagttgatg atgtcgacgt accgctagta acgggagctc cactctgtaa 1680
297 tttggtatgc gtcccatttt aagtgaacgg tgttcccatg aactcgtgtt cccatacaaa 1740
298 gccgtgcagc gaataccttc tcaataggtt attgaaaact taattgcgtg tgttgactga 1800
299 gtcacttgtg taaaattgat gaaaaaataa gcagtgcgaa tttatcttta gggacggttc 1860
300 tattctacac acaaaaaagt aagtttggtt aaaacaatga tttcaaaaga aatttgattt 1920
301 atacagtttc cagcgtagca atgataaata catgtgtcaa caactcgaaa acgaactaca 1980
302 atatttcaat atttcatcat tccgtcaatt ctgtcatttt ataaaaaat tgtttcaagc 2040
303 gaacagataa gctaaagcta aggtatagtt ataataaat aatgttaaat acataaaaag 2100
304 tcaaaaaccc gaacaagtgg cgaatggtaa acccgttccg agcgttcata cggttttggt 2160
305 tctatttcct gctcctctgg gggtagttgc tgact 2195
308 <210> SEQ ID NO: 17
309 <211> LENGTH: 227
310 <212> TYPE: PRT
311 <213> ORGANISM: Drosophila melanogaster
313 <400> SEQUENCE: 17
314 Met Glu Lys Ser Phe Pro Ile Thr Pro Trp Lys Tyr Gly Leu Leu Val
315 1 5 10 15
317 Thr Cys Ile Leu Ile Val Thr Cys Asn Val Phe Phe Phe Ser Cys Gly
318 20 25 30
320 Val Thr Thr Trp Gly Ser Ala Val Ser Val Tyr Gly Ser Tyr Gly Ser
321 35 40 45
323 Ala Leu Cys Gly Gly Ala Val Phe Gly Val Ala Phe Leu Gly Met Tyr
324 50 55 60
326 Val Ala Leu Lys Val Ser Tyr Lys Tyr Ser Ile Tyr Tyr Leu Ile Cys
327 65 70 75 80
329 Ser Gly Leu Val Ile Ala Ala Leu Gly Ser Tyr Leu Phe Thr Phe Thr
330 85 90 95
332 Ala Met Arg Glu Gln Leu Met Gly Arg Phe Glu Glu Arg Met Arg Asp

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/761,142  
 DATE: 01/30/2001  
 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

```

205 acgcggatct gcagcagacc cccgaccacc tctatctgga cgggtgcate gaaaaggtgc 660
206 agagcttcta cgaagcagac aagctgcgct lcatcatagt gtcctgggtg ctagtggcct 720
207 tcgagttaat ctgcttcgcc ttggccgtgt ttctggccat tagttttaag aacaagcagc 780
208 gacggatgga gttctagttc taggcttcgg taatctcgag ctatccaaca gtacaaactc 840
209 ggaatcgggg tctcgctgat atttttctct tcaacatttc ataaccaaat gcaaaggaca 900
210 gtcataaatt attcaactct acctaatgt aacctgtaat taaagtacat attttagatt 960
211 caattaccca ttataagtat cataataaat gtgcgcgtgt ttgttttcac atga 1014
214 <210> SEQ ID NO: 15
215 <211> LENGTH: 208
216 <212> TYPE: PRT
217 <213> ORGANISM: Drosophila melanogaster
219 <400> SEQUENCE: 15
220 Met Gly Cys Ala Thr Thr Ser Val Lys Ile Ala Ser Ile Val Leu Asn
221 1 5 10 15
223 Ala Val Leu Gly Phe Leu Ala Ala Gly Ala Ile Gly Trp Ile Ala Tyr
224 20 25 30
226 Asn Ala Asp Thr Glu Thr Glu Glu Phe Val Ile Ala Ala Tyr Ile Ala
227 35 40 45
229 Cys Ser Leu Ile Leu Val Phe Ala Leu Leu Gly Ile Phe Ala Ala Ile
230 50 55 60
232 Arg Glu Ser Val Val Leu Thr Ala Thr Ser Ala Val Phe Leu Leu Ile
233 65 70 75 80
235 Leu Ala Ile Leu Gln Ile Val Ser Thr Cys Leu Phe Leu His Glu Phe
236 85 90 95
238 Asp Val Lys Ser Gly Arg Asp Met Val Glu Val Ala Trp Gln Ala Asn
239 100 105 110
241 Asn Met Asp Ser Leu Gln Gln Lys His Glu Cys Cys Gly Gln Ser Ser
242 115 120 125
244 Ala Gln Asp Tyr Ile His Leu Ser Leu Leu Ile Pro Pro Ser Cys Tyr
245 130 135 140
247 Ala Asp Leu Gln Gln Thr Pro Asp His Leu Tyr Leu Asp Gly Cys Ile
248 145 150 155 160
250 Glu Lys Val Gln Ser Phe Tyr Glu Ser Asp Lys Leu Arg Phe Ile Ile
251 165 170 175
253 Val Ser Trp Val Leu Val Ala Phe Glu Leu Ile Cys Phe Ala Leu Ala
254 180 185 190
256 Val Phe Leu Ala Ile Ser Phe Lys Asn Lys Gln Arg Arg Met Glu Phe
257 195 200 205
263 <210> SEQ ID NO: 16
264 <211> LENGTH: 2195
265 <212> TYPE: DNA
266 <213> ORGANISM: Drosophila melanogaster
268 <400> SEQUENCE: 16
269 tacctcttca gcaaagggtt ttgtggggacc ttcattgcgg atgaccagtg gacgtaagag 60
270 taacaccatt cactttttct acgcgtaaag gggtaaggtc tcgaaaagggt aaaagggctc 120
271 ggactggggt taccttaga acgtgttgtg ggccactacg ctcgttactc ggttttagct 180
272 ttttagttat aacgcgggtt caagtgtaga aagcgttctc tcgtttttta ccaactgttac 240
273 tcggcgattt ctgatatttg ttttagctacg ttagagtttt ttataaatat ttacgtatta 300
274 tggacaagtg tatgaatgta ttaaggcggc cggtcgacaa acattaaaaa cgttatagat 360

```

RAW SEQUENCE LISTING                      DATE: 01/30/2001  
 PATENT APPLICATION: US/09/761,142        TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

```

139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
144     Sequence Sp3
146 <400> SEQUENCE: 10
147 gagtacgcaa agctttaact atgt                24
150 <210> SEQ ID NO: 11
151 <211> LENGTH: 23
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
157     Sequence Sp6
159 <400> SEQUENCE: 11
160 tgaccacatc caaacatcct ctt                23
163 <210> SEQ ID NO: 12
164 <211> LENGTH: 25
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
170     Sequence Sp5
172 <400> SEQUENCE: 12
173 gcatcacaaa aatcgacgct caagt                25
176 <210> SEQ ID NO: 13
177 <211> LENGTH: 19
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
183     Sequence Spe1
185 <400> SEQUENCE: 13
186 gacactcaga atactattc                19
189 <210> SEQ ID NO: 14
190 <211> LENGTH: 1014
191 <212> TYPE: DNA
192 <213> ORGANISM: Drosophila melanogaster
194 <400> SEQUENCE: 14
195 agcgaacgca gaacgcgccca gaccaaaaag ttcagattcg agagcggata tcccgccgag 60
196 cgttcacgga aalatatttg ttgttatcgc ggtccagca acgaatattt aaataaaca 120
197 aaaacgaact ttattcgtgt gcggagagag aagtcaaaa atcccaataa atgggttgcg 180
198 ccacgaccag cgtgaagatc gctccatcgc ttctgaatgc cgttttaggg ttctttgctg 240
199 ctggggccat cggttgata gcttacaatg cggacacgga gacggaggaa ttctgaatag 300
200 ccgcttacat cgcgtgctcg ctcactctgg tctttgctct gctgggcac ttccgcggca 360
201 tccgggaatc ggtggtgctg actgcaacga gtgctgtctt cctgctgac ttggccatcc 420
202 tgcagatcgt gacacactgc ctgttctctc acgagttcga cgtgaagagc ggccgggaca 480
203 tgggtggaggt ggccctggcag gcgaacaaca tggattcctt gcagcagaag cacgagtgtc 540
204 gcggccagag cagcgccag gactatatcc acctcagcct gctgatcccg cccagctgct 600

```

RAW SEQUENCE LISTING                      DATE: 01/30/2001  
 PATENT APPLICATION: US/09/761,142        TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

```

68 <400> SEQUENCE: 4
69 ccttagcatg tccgtggggt ttgaat
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 28
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
79     Sequence Pry2
81 <400> SEQUENCE: 5
82 cttgcgcgacg ggaccacatt atgttatt
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 19
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
92     Sequence Plw3-1
94 <400> SEQUENCE: 6
95 tgtcggcgtc atcaactcc
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 29
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
105     Sequence Pwht1
107 <400> SEQUENCE: 7
108 gtaacgctaa tcactccgaa caggtcaca
111 <210> SEQ ID NO: 8
112 <211> LENGTH: 25
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
118     Sequence Splac2
120 <400> SEQUENCE: 8
121 gaattcactg gccgtcgttt tacaa
124 <210> SEQ ID NO: 9
125 <211> LENGTH: 22
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
131     Sequence Spl
133 <400> SEQUENCE: 9
134 acacaacctt tcctctcaac aa
137 <210> SEQ ID NO: 10
138 <211> LENGTH: 24

```

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/76/142

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)     . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                         (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                         This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism      Sequence(s)      are missing this mandatory field or its response.  
(NEW RULES)
- 12      Use of <220>Feature      Sequence(s)      are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001

TIME: 11:19:34

Input Set : A:\31133A.ST25.txt

Output Set: N:\CRF3\01302001\I761142.raw

Does Not Comply  
Corrected Diskette Needed

P. 6

OK -->

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3 <110> APPLICANT: Kamdar, Kim
4   Broadus, Julie
5   Stam, Lynn
6   Bachmann, Jane
8 <120> TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
9   PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
11 <130> FILE REFERENCE: PB/5-31133A
13 <140> CURRENT APPLICATION NUMBER: US/09/761,142
13 <141> CURRENT FILING DATE: 2001-01-16
13 <150> PRIOR APPLICATION NUMBER: US 60/176,418
14 <151> PRIOR FILING DATE: 2000-01-14
16 <160> NUMBER OF SEQ ID NOS: 361
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 27
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
27   Sequence Plac4
29 <400> SEQUENCE: 1
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33 <210> SEQ ID NO: 2
34 <211> LENGTH: 24
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
40   Sequence Plac1
42 <400> SEQUENCE: 2
43 caccacaaggc tctgtctccca caat
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 23
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
53   Sequence Pry4
55 <400> SEQUENCE: 3
56 caatcatatc gctgtctcac tca
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 26
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
66   Sequence Pry1

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27

24

23